

1. (Cancelled)
2. (Currently amended) The γ -proteobacterium according to claim 10, wherein said ArcA protein is selected from the group consisting of:
 - (A) a protein comprising the amino acid sequence of SEQ ID NO: 32; and
 - (B) a protein comprising up to 10 amino acid substitutions, deletions, or insertions in the amino acid sequence of SEQ ID NO: 32.
3. (Currently amended) The γ -proteobacterium according to claim 10, wherein said ArcA protein is selected from the group consisting of:
 - (A) a protein comprising the amino acid sequence of SEQ ID NO: 32; and
 - (B) a protein comprising an amino acid sequence which is at least 70% homologous to SEQ ID NO: 32.
4. (Cancelled)
5. (Currently amended) The γ -proteobacterium according to claim 10, wherein said production of the ArcA protein is reduced or eliminated by disruption of an *arcA* gene on a chromosome.
6. (Currently amended) The γ -proteobacterium according to claim 5, wherein said *arcA* gene is selected from the group consisting of:
 - (a) DNA containing the nucleotide sequence of the nucleotide number 101 to 817 of SEQ ID NO: 31; and
 - (b) DNA which is able to hybridize with the nucleotide sequence of the nucleotide numbers 101 to 817 of SEQ ID NO: 31 under stringent conditions comprising washing at a salt concentration of 1 x SSC, 0.1% SDS at 65° C.
7. (Currently amended) The γ -proteobacterium according to claim 10, comprising a bacterium belonging to the genus *Escherichia*.
8. (Currently amended) The γ -proteobacterium according to claim 10, wherein said target substance comprises an L-amino acid.
9. (Currently amended) The γ -proteobacterium according to claim 8, wherein said L-amino acid is selected from the group consisting of L-lysine, L-glutamic acid, L-arginine, and L-threonine.
10. (Currently amended) A method for producing a target substance synthesized via the tricarboxylic acid cycle comprising:

(a) culturing the γ -proteobacterium wherein production of ArcA protein is reduced or eliminated, and wherein said γ -proteobacterium has an improved ability to produce a target substance synthesized via the tricarboxylic acid cycle as compared to a wild-type γ -proteobacterium according to claim 1 in a medium; and

(b) collecting said target substance from the culture.